CLAIMS

We claim:

1. A method for detecting, or for detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof in a subject comprising:

obtaining, from the subject, a biological sample; and

determining, using a suitable assay, the expression level of at least one gene or sequence selected from the group consisting of: ZNF185 (SEQ ID NOS:1 and 2); PSP94 (SEQ ID NOS:29 and 30); BPAG1 (SEQ ID NO:31); SORBS1 (SEQ ID NOS:32 and 33); C21orf63 (SEQ ID NO:34); SVIL (SEQ ID NOS:35 and 36); PRIMA1 (SEQ ID NO:37); FLJ14084 (SEQ ID NOS:38 and 39); TU3A (SEQ ID NOS:40 and 41); KIAA1210 (SEQ ID NO:42); SOX4 (SEQ ID NOS:43 and 44); MLP (SEQ ID NOS:45 and 46); FABP5 (SEQ ID NOS:47 and 48); MAL2 (SEQ ID NOS:49 and 50); Erg-2 (SEQ ID NOS: 51 and 52); and sequences that hybridize under high stringency thereto, whereby detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof is, at least in part, afforded.

2. The method according to claim 1, wherein said expression level is determined by detecting the presence, absence or level of mRNA transcribed from said gene or sequence.

3. The method according to claim 1, wherein said expression level is determined by detecting the presence, absence or level of a polypeptide encoded by said gene or sequence.

4. The method according to claim 1, wherein detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof is, at least in part, based on a *decrease* in expression of at least one gene or sequence selected from the group consisting of: ZNF185 (SEQ ID NOS:1 and 2); PSP94 (SEQ ID NOS:29 and 30); BPAG1 (SEQ ID NO:31); SORBS1 (SEQ ID NOS:32 and 33); C21orf63 (SEQ ID NO:34); SVIL (SEQ ID NOS:35 and 36); PRIMA1 (SEQ ID NO:37); FLJ14084 (SEQ ID NOS:38 and 39); TU3A (SEQ ID NOS:40 and 41); KIAA1210 (SEQ ID NO:42); and sequences that hybridize under high stringency thereto.

5. The method according to claim 1, wherein detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof is, at least in part, based on a *increase* in expression of at least one gene or sequence selected from the group consisting of: SOX4 (SEQ ID

NOS:43 and 44); MLP (SEQ ID NOS:45 and 46); FABP5 (SEQ ID NOS:47 and 48); MAL2 (SEQ ID NOS:49 and 50); Erg-2 (SEQ ID NOS: 51 and 52); and sequences that hybridize under high stringency thereto.

6. The method according to claim 3, wherein said polypeptide is detected by at least one method selected from the group consisting of immunoassay, ELISA immunoassay, radioimmunoassay, and antibody.

7. The method according to claim 1 wherein said expression is determined by detecting the presence or absence of CpG methylation within said gene or sequence, wherein hypermethylation indicates the presence of, or stage of the prostate cell proliferative disorder.

8. The method according to claim 7, wherein expression is of at least one gene or sequence selected from the group consisting of: ZNF185 (SEQ ID NOS:1 and 2); SVIL (SEQ ID NOS:35 and 36); PRIMA1 (SEQ ID NO:37); FLJ14084 (SEQ ID NOS:38 and 39); TU3A (SEQ ID NOS:40 and 41); KIAA1210 (SEQ ID NO:42); and sequences that hybridize under high stringency thereto.

9. A method for detecting, or for detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof in a subject, comprising:

obtaining, from the subject, a biological sample having genomic DNA; and

contacting genomic DNA obtained from the subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides within at least one target region of the genomic DNA, wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of at least one sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein said contiguous nucleotides comprise at least one CpG dinucleotide sequence, and whereby detecting, or detecting and distinguishing between or among colon cell proliferative disorders or stages thereof is, at least in part, afforded.

10. The method of claim 9, wherein normal, non-prostate cell proliferative disorders, or adjacent benign tissues are distinguished from at least one condition selected from the group consisting of: intermediate, T2, Gleason score 6 lymph node positive and negative; high grade,T3,

Gleason score 9 lymph node positive and negative; prostatic adenocarcinoma; and metastatic tumors.

11. The method of claim 9, wherein adjacent benign tissue is distinguished from at least one condition selected from the group consisting of: intermediate, T2, Gleason score 6 lymph node positive and negative; high grade,T3, Gleason score 9 lymph node positive and negative; prostatic adenocarcinoma; and metastatic tumors.

12. The method of claim 9, wherein adjacent benign tissue is distinguished from at least one condition selected from the group consisting of: intermediate, T2, Gleason score 6 lymph node positive and negative; high grade,T3, Gleason score 9 lymph node positive and negative; prostatic adenocarcinoma; and metastatic tumors, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of ZNF185 (SEQ ID NO:1); PSP94 (SEQ ID NO:29); BPAG1 (SEQ ID NO:31); SORBS1 (SEQ ID NO:32); C21orf63 (SEQ ID NO:34); SVIL (SEQ ID NS:35); PRIMA1 (SEQ ID NO:37); FLJ14084 (SEQ ID NO:38); TU3A (SEQ ID NO:40); KIAA1210 (SEQ ID NO:42); and sequences complementary thereto.

13. The method of claim 12, wherein adjacent benign tissue is distinguished from at least one condition selected from the group consisting of: intermediate, T2, Gleason score 6 lymph node positive and negative; high grade,T3, Gleason score 9 lymph node positive and negative; prostatic adenocarcinoma; and metastatic tumors, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of ZNF185 (SEQ ID NO:1); SVIL (SEQ ID NO:35); PRIMA1 (SEQ ID NO:37); FLJ14084 (SEQ ID NO:38); TU3A (SEQ ID NO:40); KIAA1210 (SEQ ID NO:42); and sequences complementary thereto.

14. The method of claim 9, wherein tissues originating from the prostate are distinguished from tissues of non-prostate origin.

15. The method of claim 9, wherein prostate cell proliferative disorders are distinguished from healthy tissues, and wherein the target region comprises, or hybridizes under stringent conditions to at least 16 contiguous nucleotides of a sequence selected from the group consisting of ZNF185 (SEQ ID NO:1); PSP94 (SEQ ID NO:29); BPAG1 (SEQ ID NO:31); SORBS1 (SEQ ID

NO:32); C21orf63 (SEQ ID NO:34); SVIL (SEQ ID NO:35); PRIMA1 (SEQ ID NO:37); FLJ14084 (SEQ ID NO:38); TU3A (SEQ ID NO:40); KIAA1210 (SEQ ID NO:42); and sequences complementary thereto.

16. A method for detecting, or for detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof in a subject, comprising:

obtaining, from a subject, a biological sample having genomic DNA;

contacting the genomic DNA, or a fragment thereof, with one reagent or a plurality of reagents that distinguishes between methylated and non methylated CpG dinucleotide sequences within at least one target sequence of the genomic DNA, or fragment thereof, wherein the target sequence comprises, or hybridizes under stringent conditions to, at least 16 contiguous nucleotides of a sequence taken from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and

determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences, whereby detecting, or detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof is, at least in part, afforded.

17. The method of claim 16, wherein detecting, or detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof comprises detecting, or detecting and distinguishing between or among one or more tissues selected from the group consisting of: adjacent benign tissues; intermediate, T2, Gleason score 6 lymph node positive or negative tissue; high grade, T3, Gleason score 9 lymph node positive or negative tissue; prostatic adenocarcinoma; and metastatic tumors.

18. The method of claim 16, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises converting unmethylated cytosine bases within the target sequence to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties.

19. The method of claim 16, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence(s) comprises methylation state-dependent conversion or non-conversion of at least one CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence.

20. The method of claim 16, wherein the biological sample is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.

21. The method of claim 16, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises use of at least one nucleic acid molecule or peptide nucleic acid (PNA) molecule comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

22. The method of claim 21, wherein the contiguous sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.

23. The method of claim 21, comprising use of at least two such nucleic acid molecules, or peptide nucleic acid (PNA) molecules.

24. The method of claim 21, comprising use of at least two such nucleic acid molecules as primer oligonucleotides for the amplification of a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51; sequences that hybridize under stringent conditions therto; and complements thereof.

25. The method of claim 21, comprising use of at least four such nucleic acid molecules, peptide nucleic acid (PNA) molecules.

26. A method for detecting, or detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof in a subject, comprising:

obtaining, from a subject, a biological sample having genomic DNA;

extracting or otherwise isolating the genomic DNA;

treating the genomic DNA, or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence of at least 9 nucleotides that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein the treated genomic DNA or the fragment thereof is either amplified to produce at least one amplificate, or is not amplified; and

determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, or an average, or a value reflecting an average methylation state of a plurality of said CpG dinucleotides, whereby at least one of detecting, and detecting and distinguishing between prostate cell proliferative disorders or stages thereeof is, at least in part, afforded.

27. The method of claim 26, wherein treating the genomic DNA, or the fragment thereof comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.

28. The method of claim 26, wherein contacting or amplifying comprises use of at least one method selected from the group consisting of: use of a heat-resistant DNA polymerase as the amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid molecule carrying a detectable labels; and combinations thereof.

29. The method of claim 28, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

30. The method of claim 26, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.

31. The method of claim 26, wherein detecting, or detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof comprises detecting, or detecting and distinguishing between or among one or more tissues selected from the group consisting of: adjacent benign tissues; intermediate, T2, Gleason score 6 lymph node positive or negative tissue; high grade, T3, Gleason score 9 lymph node positive or negative tissue; prostatic adenocarcinoma; and metastatic tumors.

32. The method of claim 26, further comprising for the step of contacting the treated genomic DNA, the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized.

33. The method of claim 32, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case modified at the 5'-end thereof to preclude degradation by an enzyme having 5'-3' exonuclease activity.

34. The method of claim 32, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case lacking a 3' hydroxyl group.

35. The method of claim 32, wherein the amplification enzyme is a polymerase lacking 5'-3' exonuclease activity.

36. The method of claim 26, wherein determining comprises hybridization of at least one nucleic acid molecule or peptide nucleic acid molecule in each case comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

37. The method of claim 36, wherein at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase.

38. The method of claim 36, wherein a plurality of such hybridizing nucleic acid molecules or peptide nucleic acid molecules are bound to a solid phase in the form of a nucleic acid or peptide nucleic acid array selected from the array group consisting of linear or substantially so, hexagonal or substantially so, rectangular or substantially so, and combinations thereof.

39. The method of claim 36, further comprising extending at least one such hybridized nucleic acid molecule by at least one nucleotide base.

40. The method of claim 26, wherein determining comprises sequencing of the amplificate.

41. The method of claim 26, wherein contacting or amplifying comprises use of methylation-specific primers.

42. The method of claim 26, comprising, for the contacting step, using primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides; and further comprising, for the determining step, the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing, in the determining step, of the amplificate.

43. The method of claim 26 comprising, for the contacting step, use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized; and further comprising, in the determining step, the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing, in the determining step, of the amplificate.

44. The method of claim 26, comprising, in the contacting step, amplification by primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides and further comprising, in the determining step, hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

45. The method of claim 26, comprising, in the contacting step, the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized, and further comprising, in the determining step, hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

46. A method for detecting, or for detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof in a subject, comprising:

obtaining, from a subject, a biological sample having genomic DNA;

extracting, or otherwise isolating the genomic DNA;

contacting the genomic DNA, or a fragment thereof, comprising at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, complements thereof; and sequences that hybridize under stringent conditions thereto, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is, with respect to each cleavage recognition motif thereof, either cleaved thereby to produce cleavage fragments, or not cleaved thereby; and

determining, based on a presence or absence of, or on property of at least one such cleavage fragment, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51; and complements thereof, or an average, or a value reflecting an average methylation state of a plurality of said CpG dinucleotides, whereby at least one of detecting, or of detecting and differentiating between or among prostate cell proliferative disorders or stages thereof is, at least in part, afforded.

47. The method of claim 46, further comprising, prior to determining, amplifying of the digested or undigested genomic DNA.

48. The method of claim 47, wherein amplifying comprises use of at least one method selected from the group consisting of: use of a heat resistant DNA polymerase as an amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid carrying a detectable label; and combinations thereof.

49. The method of claim 48, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

50. The method of claim 46, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.

51. An isolated treated nucleic acid derived from SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

52. A nucleic acid, comprising at least 16 contiguous nucleotides of a treated genomic DNA sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

53. The nucleic acid of claims 52, wherein the contiguous base sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.

54. The nucleic acid of any one of claims 52 and 53, wherein the treatment comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.

55. An oligomer, comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

56. The oligomer of claim 55, comprising at least one CpG , CpA or TpG dinucleotide sequence.

57. A set of oligomers, comprising at least two oligonucleotides according, in each case, to any one of claims 55 or 56.

58. The use of a set of oligonucleotides according to claim 57 for at least one of: detection of; detection and differentiation between or among subclasses or stages of; diagnosis of; prognosis of; treatment of; monitoring of; and treatment and monitoring of prostate cell proliferative disorders.

59. The use of a nucleic acid according to any one of claims 52 through 54, an oligonucleotide according to any one of claims 55 or 56, or a set of oligonucleotides according to claim 57 for detecting, or detecting and distinguishing between or among prostate cell proliferative disorders or stages thereof selected from the group consisting of: adjacent benign tissues; intermediate, T2, Gleason score 6 lymph node positive or negative tissue; high grade, T3, Gleason score 9 lymph node positive or negative tissue; prostatic adenocarcinoma; and metastatic tumors.

60. Use of a set of oligomers according, in each case, to claim 57 as probes for determining at least one of a cytosine methylation state, and a single nucleotide polymorphism (SNP) of a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and sequences complementary thereto.

61. The use of claim 60, wherein at least two oligomers according to any one of claims 55 or 56, are used as primer oligonucleotides for the amplification of a DNA sequence of at least 16 contiguous nucleotides of a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

62. Use of a nucleic acid according to any one of claims 52-54 for determination of at least one of cytosine methylation status of a corresponding genomic DNA, or detection of a single nucleotide polymorphism (SNP).

63. A method for manufacturing a nucleic acid array, comprising at least one of attachment of an oligomer according to any one of claims 55 or 56, or attachment of a set of oligomers or nucleic acids according to claim 57, to a solid phase.

64. An oligomer array manufactured according to Claim 79.

65. The oligomer array of claim 64, wherein the oligomers are bound to a planar solid phase in the form of a lattice selected from the group consisting of linear or substantially linear lattice, hexagonal or substantially hexagonal lattice, rectangular or substantially rectangular lattice, and lattice combinations thereof.

66. Use of the oligomer array of claim 64 for the analysis of prostate cell proliferative disorders.

67. The array of claim 64, wherein the solid phase surface comprises a material selected from the group consisting of silicon, glass, polystyrene, aluminum, steel, iron, copper, nickel, silver, gold, and combinations thereof.

68. A kit useful for detecting, or for detecting distinguishing between or among prostate cell proliferative disorders or stages thereof of a subject, comprising: at least one of a bisulfite reagent, and a methylation-sensitive restriction enzyme; and at least one nucleic acid molecule or peptide nucleic acid molecule comprising, in each case a contiguous sequence at least 9 nucleotides that is complementary to, or hybridizes under stringent conditions to a bisulfite-converted sequence derived from a sequence selected from the group consisting of SEQ ID NOS:1, 29, 31, 32, 34, 35, 37, 38, 40, 42, 43, 45, 47, 49, 51, and complements thereof.

69. The kit of claim 68, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, COBRA, nucleic acid sequencing, and combinations thereof.

70. The method of any one of claims 9, 16, 26 or 46, comprising use of the kit according to claim 68.

71. Use of a nucleic acid according to any one of claims 52 through 54, an oligomer according to any one of claims 55 or 56, a set of oligonucleotides according to claim 57, a method of manufacturing according to claim 63, an array according to any one of claims 64 or 65, and a kit according to any one of claims 68 or 69 for the detection of, detection and differentiation between or among subclasses or stages of, diagnosis of, prognosis of, treatment of, monitoring of, or treatment and monitoring of prostate cell proliferative disorders.